

Asp	Leu	Gln	Leu	Arg	Cys	Arg	Leu	Arg	Asp	Asp	Val	Gln	Ser	Ile	
50					55				60						
Asn	Trp	Leu	Arg	Asp	Gly	Val	Gln	Leu	Ala	Glu	Ser	Asn	Arg	Thr	Arg
65					70					75					80
Ile	Thr	Gly	Glu	Glu	Val	Glu	Val	Gln	Asp	Ser	Val	Pro	Ala	Asp	Ser
				85					90					95	
Gly	Leu	Tyr	Ala	Cys	Val	Thr	Ser	Ser	Pro	Ser	Gly	Ser	Asp	Thr	Thr
			100					105					110		
Tyr	Phe	Ser	Val	Asn	Val	Ser	Asp	Ala	Leu	Pro	Ser	Ser	Glu	Asp	Asp
		115					120					125			
Asp	Asp	Asp	Asp	Asp	Ser	Ser	Ser	Glu	Glu	Lys	Glu	Thr	Asp	Asn	Thr
	130					135					140				
Lys	Pro	Asn	Pro	Val	Ala	Pro	Tyr	Trp	Thr	Ser	Pro	Glu	Lys	Met	Glu
145					150					155					160
Lys	Lys	Leu	His	Ala	Val	Pro	Ala	Ala	Lys	Thr	Val	Lys	Phe	Lys	Cys
				165					170					175	
Pro	Ser	Ser	Gly	Thr	Pro	Asn	Pro	Thr	Leu	Arg	Trp	Leu	Lys	Asn	Gly
			180					185					190		
Lys	Glu	Phe	Lys	Pro	Asp	His	Arg	Ile	Gly	Gly	Tyr	Lys	Val	Arg	Tyr
		195					200					205			
Ala	Thr	Trp	Ser	Ile	Ile	Met	Asp	Ser	Val	Val	Pro	Ser	Asp	Lys	Gly
						215					220				
Asn	Tyr	Thr	Cys	Ile	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Ile	Asn	His	Thr
225					230					235					240
Tyr	Gln	Leu	Asp	Val	Val	Glu	Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln
				245					250					255	
Ala	Gly	Leu	Pro	Ala	Asn	Lys	Thr	Val	Ala	Leu	Gly	Ser	Asn	Val	Glu
			260					265					270		
Phe	Met	Cys	Lys	Val	Tyr	Ser	Asp	Pro	Gln	Pro	His	Ile	Gln	Trp	Leu
		275					280					285			
Lys	His	Ile	Glu	Val	Asn	Gly	Ser	Lys	Ile	Gly	Pro	Asp	Asn	Leu	Pro
	290					295					300				
Tyr	Val	Gln	Ile	Leu	Lys	Thr	Ala	Gly	Val	Asn	Thr	Thr	Asp	Lys	Glu
305					310					315					320
Met	Glu	Val	Leu	His	Leu	Arg	Asn	Val	Ser	Phe	Glu	Asp	Ala	Gly	Glu
				325					330					335	
Tyr	Thr	Cys	Leu	Ala	Gly	Asn	Ser	Ile	Gly	Leu	Ser	His	His	Ser	Ala
			340					345					350		
Trp	Leu	Thr	Val	Leu	Glu	Ala	Leu	Glu	Glu	Arg	Pro	Ala	Val	Met	Thr
			355				360					365			
Ser	Pro	Leu	Tyr	Leu	Glu	Ile	Ile	Ile	Tyr	Cys	Thr	Gly	Ala	Phe	Leu
						375					380				
Ile	Ser	Cys	Met	Val	Gly	Ser	Val	Ile	Val	Tyr	Lys	Met	Lys	Ser	Gly
385					390					395					400
Thr	Lys	Lys	Ser	Asp	Phe	His	Ser</								

It is not a simple matter to determine the value of the α parameter in the α - β model. The value of α is determined by the relative rates of the two processes, α and β , and the relative rates of the two processes are determined by the relative rates of the two processes, α and β .

405										410					415						
Lys	Ser	Ile	Pro	Leu	Arg	Arg	Gln	Val	Thr	Val	Ser	Ala	Asp	Ser	Ser						
			420					425					430								
Ala	Ser	Met	Asn	Ser	Gly	Val	Leu	Leu	Val	Arg	Pro	Ser	Arg	Leu	Ser						
		435					440					445									
Ser	Ser	Gly	Thr	Pro	Met	Leu	Ala	Gly	Val	Ser	Glu	Tyr	Glu	Leu	Pro						
		450				455					460										
Glu	Asp	Pro	Arg	Trp	Glu	Leu	Pro	Arg	Asp	Arg	Leu	Val	Leu	Gly	Lys						
465					470					475					480						
Pro	Leu	Gly	Glu	Gly	Cys	Phe	Gly	Gln	Val	Val	Leu	Ala	Glu	Ala	Ile						
				485					490					495							
Gly	Leu	Asp	Lys	Asp	Lys	Pro	Asn	Arg	Val	Thr	Lys	Val	Ala	Val	Lys						
			500					505					510								
Met	Leu	Lys	Ser	Asp	Ala	Thr	Glu	Lys	Asp	Leu	Ser	Asp	Leu	Ile	Ser						
		515					520					525									
Glu	Met	Glu	Met	Met	Lys	Met	Ile	Gly	Lys	His	Lys	Asn	Ile	Ile	Asn						
530						535					540										
Leu	Leu	Gly	Ala	Cys	Thr	Gln	Asp	Gly	Pro	Leu	Tyr	Val	Ile	Val	Glu						
545					550					555					560						
Tyr	Ala	Ser	Lys	Gly	Asn	Leu	Arg	Glu	Tyr	Leu	Gln	Ala	Arg	Arg	Pro						
				565					570					575							
Pro	Gly	Leu	Glu	Tyr	Cys	Tyr	Asn	Pro	Ser	His	Asn	Pro	Glu	Glu	Gln						
			580					585					590								
Leu	Ser	Ser	Lys	Asp	Leu	Val	Ser	Cys	Ala	Tyr	Gln	Val	Ala	Arg	Gly						
		595					600					605									
Met	Glu	Tyr	Leu	Ala	Ser	Lys	Lys	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala						
610						615					620										
Arg	Asn	Val	Leu	Val	Thr	Glu	Asp	Asn	Val	Met	Lys	Ile	Ala	Asp	Phe						
625					630					635					640						
Gly	Leu	Ala	Arg	Asp	Ile	His	His	Ile	Asp	Tyr	Tyr	Lys	Lys	Thr	Thr						
				645					650					655							
Asn	Gly	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ala	Leu	Phe	Asp						
			660					665					670								
Arg	Ile	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu						

Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg Ser Ser
770 775 780

Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro Leu Pro
785 790 795 800

Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn Gly Gly
805 810 815

Leu Lys Arg Arg
820

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
1 5 10 15
Thr Leu Cys Thr Ala Arg Pro Ser Pro Thr Leu Pro Glu Gln Ala Gln
20 25 30
Pro Trp Gly Ala Pro Val Glu Val Glu Ser Phe Leu Val His Pro Gly
35 40 45
Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
50 55 60
Asn Trp Leu Arg Asp Gly Val Gln Leu Ala Glu Ser Asn Arg Thr Arg
65 70 75 80
Ile Thr Gly Glu Glu Val Glu Val Gln Asp Ser Val Pro Ala Asp Ser
85 90 95
Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
100 105 110
Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
115 120 125
Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
130 135 140
Lys Pro Asn Arg Met Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
145 150 155 160
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
165 170 175
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
180 185 190
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
195 200 205

U5620561.072000

09060501.070000

Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
210 215 220

Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
225 230 235 240

His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
245 250 255

Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn
260 265 270

Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
275 280 285

Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
290 295 300

Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
305 310 315 320

Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
325 330 335

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
340 345 350

Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
355 360 365

Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
370 375 380

Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys
385 390 395 400

Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
405 410 415

Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
420 425 430

Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
435 440 445

Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
450 455 460

Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
465 470 475 480

Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
485 490 495

Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
500 505 510

Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
515 520 525

Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
530 535 540

Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
545 550 555 560

Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg

565										570					575						
Arg	Pro	Pro	Gly	Leu	Glu	Tyr	Cys	Tyr	Asn	Pro	Ser	His	Asn	Pro	Glu						
			580					585					590								
Glu	Gln	Leu	Ser	Ser	Lys	Asp	Leu	Val	Ser	Cys	Ala	Tyr	Gln	Val	Ala						
		595					600					605									
Arg	Gly	Met	Glu	Tyr	Leu	Ala	Ser	Lys	Lys	Cys	Ile	His	Arg	Asp	Leu						
	610					615					620										
Ala	Ala	Arg	Asn	Val	Leu	Val	Thr	Glu	Asp	Asn	Val	Met	Lys	Ile	Ala						
625					630					635					640						
Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	His	His	Ile	Asp	Tyr	Tyr	Lys	Lys						
				645					650					655							
Thr	Thr	Asn	Gly	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ala	Leu						
			660					665					670								
Phe	Asp	Arg	Ile	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val						
		675					680					685									
Leu	Leu	Trp	Glu	Ile	Phe	Thr	Leu	Gly	Gly	Ser	Pro	Tyr	Pro	Gly	Val						
		690					695				700										
Pro	Val	Glu	Glu	Leu	Phe	Lys	Leu	Leu	Lys	Glu	Gly	His	Arg	Met	Asp						
705					710					715					720						
Lys	Pro	Ser	Asn	Cys	Thr	Asn	Glu	Leu	Tyr	Met	Met	Met	Arg	Asp	Cys						
				725					730					735							
Trp	His	Ala	Val	Pro	Ser	Gln	Arg	Pro	Thr	Phe	Lys	Gln	Leu	Val	Glu						
			740					745						750							
Asp	Leu	Asp	Arg	Ile	Val	Ala	Leu	Thr	Ser	Asn	Gln	Glu	Tyr	Leu	Asp						
		755					760					765									
Leu	Ser	Met	Pro	Leu	Asp	Gln	Tyr	Ser	Pro	Ser	Phe	Pro	Asp	Thr	Arg						
		770					775					780									
Ser	Ser	Thr	Cys	Ser	Ser	Gly	Glu	Asp	Ser	Val	Phe	Ser	His	Glu	Pro						
785					790					795					800						
Leu	Pro	Glu	Glu	Pro	Cys	Leu	Pro	Arg	His	Pro	Ala	Gln	Leu	Ala	Asn						
				805					810					815							
Arg	Gly	Leu	Lys	Arg	Arg																
			820																		

(i) SEQUENCE/CHARACTERISTICS:

- (A) LENGTH: 731 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

/(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
1 5 10 15

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Trp	Ser	Trp	Lys	Cys	Leu	Leu	Phe	Trp	Ala	Val	Leu	Val	Thr	Ala
1				5					10					15	
Thr	Leu	Cys	Thr	Ala	Arg	Pro	Ser	Pro	Thr	Leu	Pro	Glu	Gln	Asp	Ala
			20					25					30		
Leu	Pro	Ser	Ser	Glu	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Ser	Ser	Ser	Glu
		35					40					45			
Glu	Lys	Glu	Thr	Asp	Asn	Thr	Lys	Pro	Asn	Arg	Met	Pro	Val	Ala	Pro
	50					55					60				
Tyr	Trp	Thr	Ser	Pro	Glu	Lys	Met	Glu	Lys	Lys	Leu	His	Ala	Val	Pro
65					70					75					80
Ala	Ala	Lys	Thr	Val	Lys	Phe	Lys	Cys	Pro	Ser	Ser	Gly	Thr	Pro	Asn
				85					90					95	
Pro	Thr	Leu	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu	Phe	Lys	Pro	Asp	His
			100					105					110		
Arg	Ile	Gly	Gly	Tyr	Lys	Val	Arg	Tyr	Ala	Thr	Trp	Ser	Ile	Ile	Met
		115					120						125		
Asp	Ser	Val	Val	Pro	Ser	Asp	Lys	Gly	Asn	Tyr	Thr	Cys	Ile	Val	Glu
		130				135					140				
Asn	Glu	Tyr	Gly	Ser	Ile	Asn	His	Thr	Tyr	Gln	Leu	Asp	Val	Val	Glu
145					150					155					160
Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	Ala	Asn	Lys
				165					170					175	
Thr	Val	Ala	Leu	Gly	Ser	Asn	Val	Glu	Phe	Met	Cys	Lys	Val	Tyr	Ser
			180					185					190		
Asp	Pro	Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Ile	Glu	Val	Asn	Gly
		195					200					205			
Ser	Lys	Ile	Gly	Pro	Asp	Asn	Leu	Pro	Tyr	Val	Gln	Ile	Leu	Lys	Thr
	210					215					220				
Ala	Gly	Val	Asn	Thr	Thr	Asp	Lys	Glu	Met	Glu	Val	Leu	His	Leu	Arg
225					230					235					240
Asn	Val	Ser	Phe	Glu	Asp	Ala	Gly	Glu	Tyr	Thr	Cys	Leu	Ala	Gly	Asn
				245					250					255	
Ser	Ile	Gly	Leu	Ser	His	His	Ser	Ala	Trp	Leu	Thr	Val	Leu	Glu	Ala
			260					265					270		

175

Ala	Leu	Gly	Ser	Asn	Val	Glu	Phe	Met	Cys	Lys	Val	Tyr	Ser	Asp	Pro
			180					185					190		
Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Ile	Glu	Val	Asn	Gly	Ser	Lys
		195					200					205			
Ile	Gly	Pro	Asp	Asn	Leu	Pro	Tyr	Val	Gln	Ile	Leu	Lys	Val	Ile	Met
	210					215					220				
Ala	Pro	Val	Phe	Val	Gly	Gln	Ser	Thr	Gly	Lys	Glu	Thr	Thr	Val	Ser
225					230					235					240
Gly	Ala	Gln	Val	Pro	Val	Gly	Arg	Leu	Ser	Cys	Pro	Arg	Met	Gly	Ser
				245					250					255	
Phe	Leu	Thr	Leu	Gln	Ala	His	Thr	Leu	His	Leu	Ser	Arg	Asp	Leu	Ala
			260					265					270		
Thr	Ser	Pro	Arg	Thr	Ser	Asn	Arg	Gly	His	Lys	Val	Glu	Val	Ser	Trp
		275					280					285			
Glu	Gln	Arg	Ala	Ala	Gly	Met	Gly	Gly	Ala	Gly	Leu				
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Trp	Ser	Trp	Lys	Cys	Leu	Leu	Phe	Trp	Ala	Val	Leu	Val	Thr	Ala
1				5					10					15	
Thr	Leu	Cys	Thr	Ala	Arg	Pro	Ser	Pro	Thr	Leu	Pro	Glu	Gln	Asp	Ala
			20					25					30		
Leu	Pro	Ser	Ser	Glu	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Ser	Ser	Ser	Glu
		35					40					45			
Glu	Lys	Glu	Thr	Asp	Asn	Thr	Lys	Pro	Asn	Arg	Met	Pro	Val	Ala	Pro
	50					55					60				
Tyr	Trp	Thr	Ser	Pro	Glu	Lys	Met	Glu	Lys	Lys	Leu	His	Ala	Val	Pro
65					70					75					80
Ala	Ala	Lys	Thr	Val	Lys	Phe	Lys	Cys	Pro	Ser	Ser	Gly	Thr	Pro	Asn
				85					90					95	
Pro	Thr	Leu	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu	Phe	Lys	Pro	Asp	His
			100					105					110		
Arg	Ile	Gly	Gly	Tyr	Lys	Val	Arg	Tyr	Ala	Thr	Trp	Ser	Ile	Ile	Met
		115					120					125			
Asp	Ser	Val	Val	Pro	Ser	Asp	Lys	Gly	Asn	Tyr	Thr	Cys	Ile	Val	Glu
	130					135					140				

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1. The first step is to identify the problem. This involves understanding the current situation and what needs to be changed.

(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic"

CCAACCTCTA GAGGATCCAC TGGGATGTGG AGCTGGAAGT GC

42

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "Synthetic"
```

GTAAGCGGCC GCGGATCCTT ACTACTCCAG GTACAGGGGC GA

42

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: /other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic"

CCATTGGAT CCGT/CACAGC CACACTCTGC ACCGCT

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "Synthetic"
```

Ant 30

i) SEQUENCE DESCRIPTION: SEQ ID NO:12:
GTCTG ACTTCCATCT TTTCTGGGGA TGTCCA

2

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